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TECH CENTER 1600/2900

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#3



1600

ENTERED

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/882,694B

DATE: 01/02/2003 86

TIME: 08:42:29

Input Set : A:\Seqlist.txt

Output Set: N:\CRF4\01022003\I882694B.raw

4 <110> APPLICANT: Duvick, Jon
5 Maddox, Joyce
6 Gilliam, Jacob
7 Folkerts, Otto
8 Crasta, Oswald R.
10 <120> TITLE OF INVENTION: Compositions and Methods for Fumonisin
11 Detoxification
13 <130> FILE REFERENCE: 35718/208255
15 <140> CURRENT APPLICATION NUMBER: 09/882,694B
16 <141> CURRENT FILING DATE: 2001-06-15
18 <150> PRIOR APPLICATION NUMBER: 09/351,224
19 <151> PRIOR FILING DATE: 1999-07-12
21 <160> NUMBER OF SEQ ID NOS: 33
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1691
27 <212> TYPE: DNA
28 <213> ORGANISM: Exophiala spinifera
30 <220> FEATURE:
31 <221> NAME/KEY: misc_feature
32 <222> LOCATION: (0)...(0)
33 <223> OTHER INFORMATION: flavin monooxygenase with intron
35 <400> SEQUENCE: 1
36 atgtcggcca ccagcaactc cagaggcgat tgttccgtcg catgcgacgc catcatcggtt 60
37 ggagccggcc tcagcggcat ctctgctgtg tacaaattgc gaaagctcag actcaacgcc 120
38 aaaatcttcg agggagcccc cgattttggc ggcgtctggc actggaaccg ctaccctggc 180
39 gctcgtgttg attcggagac gcccttctac caactgaaca ttcccgaagt atggaaagac 240
40 tggacctggt ctgtccgcta tcctgaccag aaagagtgc tgtcatatgt tcaccactgt 300
41 gacaagatcc ggggcttgag aaaagacgtc tacttcggag ctgaggtggt tgatgcgcgg 360
42 tatgccagag atctgggcac ctggactgtc aagacgtcgg ctggccatgt tgcgacggca 420
43 aagtatctca ttctcgctac ggggttgctc cacaggaagc aactcccgc actccccggc 480
44 ctgcgccgatt tcaacgggaa ggtgattcat tcgagtgcct ggcacgaaga cttcgacgca 540
45 gagggccaga gagtcgccgt catcgggtgc ggggccacaa gcatccagat tgttcaggag 600
46 ttggccaaga aggtcgacca ggtaaccatg tttatgcgaa ggccgagcta ttgtctgccc 660
47 atgcggcaac gaacgatgga taggaacgaa cagacagcct ggaaggccta ctaccccacg 720
48 ctgtttgaag cgagtcgaaa gtctcgatt ggattcccgg tccaggcacc gtcggttggc 780
49 atctttgaag tcagccccga gcagcgggag gcctatttcg aagagtgtg ggagcgtggg 840
50 gcctttaatt ttcttgcttg ccagtaccga gaagtcatgg ttgacaaaaa ggccaaccga 900
51 ctggtctatg acttctgggc caaaaagact cgatctcgta tcgtcaatcc ggcaaagaga 960
52 gatctcatgg ctctcttga gccgccgtac tggttcggta ccaagcgctc cccactggag 1020
53 agcgactact acgaaatgct ggacaagccg agcgtcgaaa ttgtgaatct agaacaatcg 1080
54 cccattgttg ctgttacaaa gacaggtgtg ctcttgagt acggcagcaa gagggaatgc 1140
55 gacacgatcg tgctggcgac gggtttcgac agtttctact gctcgtgagt gtgctcgatc 1200

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56 atggctccga gtccggacgt ttggctgacc ttgaaagatt gacacatatg ggcttgaaaa 1260
 57 acaagcacgg agtggacctg aaggagggtg ggaaagatgg catatctact tatatgggag 1320
 58 tcttctctca tggcttcccc aatgccttct tcgtcgccac ggctcaagcc ccgaccgtcc 1380
 59 tttccaacgg cccaacgata atagaaaccc aagtcgactt gatcgccgat acaattgcaa 1440
 60 agttggaggc cgagcacgcc acgtccgttg aggcgacgaa atcagcacia gaggcattggt 1500
 61 cgattatgat tgccaagatg aacgagcaca ctctgttccc cttgacggat tcgtggtgga 1560
 62 ctggaggcaa catccctggg aaagcaacac gtgctttaac cttcataggc gggattgctc 1620
 63 tctatgagca gatctgtcaa gagaagggtg ccaattggga tgggtttgat gtgcttcatt 1680
 64 ctccctgcta a 1691

66 <210> SEQ ID NO: 2

67 <211> LENGTH: 1638

68 <212> TYPE: DNA

69 <213> ORGANISM: Exophiala spinifera

71 <220> FEATURE:

72 <221> NAME/KEY: CDS

73 <222> LOCATION: (1)...(1638)

75 <221> NAME/KEY: misc_feature

76 <222> LOCATION: (0)...(0)

77 <223> OTHER INFORMATION: flavin monooxygenase, fully spliced

W--> 79 <400> 2

80 atg tcg gcc acc agc aac tcc aga ggc gat tgt tcc gtc gca tgc gac 48
 81 Met Ser Ala Thr Ser Asn Ser Arg Gly Asp Cys Ser Val Ala Cys Asp
 82 1 5 10 15
 84 gcc atc atc gtt gga gcc ggc ctc agc ggc atc tct gct gtg tac aaa 96
 85 Ala Ile Ile Val Gly Ala Gly Leu Ser Gly Ile Ser Ala Val Tyr Lys
 86 20 25 30
 88 ttg cga aag ctc aga ctc aac gcc aaa atc ttc gag gga gcc ccc gat 144
 89 Leu Arg Lys Leu Arg Leu Asn Ala Lys Ile Phe Glu Gly Ala Pro Asp
 90 35 40 45
 92 ttt ggc ggc gtc tgg cac tgg aac cgc tac cct ggc gct cgt gtt gat 192
 93 Phe Gly Gly Val Trp His Trp Asn Arg Tyr Pro Gly Ala Arg Val Asp
 94 50 55 60
 96 tcg gag acg ccc ttc tac caa ctg aac att ccc gaa gta tgg aaa gac 240
 97 Ser Glu Thr Pro Phe Tyr Gln Leu Asn Ile Pro Glu Val Trp Lys Asp
 98 65 70 75 80
 100 tgg acc tgg tct tgc cgc tat cct gac cag aaa gag ttg ctg tca tat 288
 101 Trp Thr Trp Ser Cys Arg Tyr Pro Asp Gln Lys Glu Leu Leu Ser Tyr
 102 85 90 95
 104 gtt cac cac tgt gac aag atc cgg ggc ttg aga aaa gac gtc tac ttc 336
 105 Val His His Cys Asp Lys Ile Arg Gly Leu Arg Lys Asp Val Tyr Phe
 106 100 105 110
 108 gga gct gag gtg gtt gat gcg cgg tat gcc aga gat ctg ggc acc tgg 384
 109 Gly Ala Glu Val Val Asp Ala Arg Tyr Ala Arg Asp Leu Gly Thr Trp
 110 115 120 125
 112 act gtc aag acg tcg gct ggc cat gtt gcg acg gca aag tat ctc att 432
 113 Thr Val Lys Thr Ser Ala Gly His Val Ala Thr Ala Lys Tyr Leu Ile
 114 130 135 140
 116 ctc gct acg ggg ttg ctc cac agg aag cac act ccc gca ctc ccc ggc 480
 117 Leu Ala Thr Gly Leu Leu His Arg Lys His Thr Pro Ala Leu Pro Gly

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```

118 145          150          155          160
120 ctc gcc gat ttc aac ggg aag gtg att cat tcg agt gcc tgg cac gaa 528
121 Leu Ala Asp Phe Asn Gly Lys Val Ile His Ser Ser Ala Trp His Glu
122          165          170          175
124 gac ttc gac gca gag ggc cag aga gtc gcc gtc atc ggt gcc ggg gcc 576
125 Asp Phe Asp Ala Glu Gly Gln Arg Val Ala Val Ile Gly Ala Gly Ala
126          180          185          190
128 aca agc atc cag att gtt cag gag ttg gcc aag aag gct gac cag gta 624
129 Thr Ser Ile Gln Ile Val Gln Glu Leu Ala Lys Lys Ala Asp Gln Val
130          195          200          205
132 acc atg ttt atg cga agg ccg agc tat tgt ctg ccc atg cgg caa cga 672
133 Thr Met Phe Met Arg Arg Pro Ser Tyr Cys Leu Pro Met Arg Gln Arg
134          210          215          220
136 acg atg gat agg aac gaa cag aca gcc tgg aag gcc tac tac ccc acg 720
137 Thr Met Asp Arg Asn Glu Gln Thr Ala Trp Lys Ala Tyr Tyr Pro Thr
138 225          230          235          240
140 ctg ttt gaa gcg agt cga aag tct cgg att gga ttc ccg gtc cag gca 768
141 Leu Phe Glu Ala Ser Arg Lys Ser Arg Ile Gly Phe Pro Val Gln Ala
142          245          250          255
144 ccg tcg gtt ggc atc ttt gaa gtc agc ccc gag cag cgg gag gcc tat 816
145 Pro Ser Val Gly Ile Phe Glu Val Ser Pro Glu Gln Arg Glu Ala Tyr
146          260          265          270
148 ttc gaa gag ttg tgg gag cgt ggg gcc ttt aat ttt ctt gct tgc cag 864
149 Phe Glu Glu Leu Trp Glu Arg Gly Ala Phe Asn Phe Leu Ala Cys Gln
150          275          280          285
152 tac cga gaa gtc atg gtt gac aaa aag gcc aac cga ctg gtc tat gac 912
153 Tyr Arg Glu Val Met Val Asp Lys Lys Ala Asn Arg Leu Val Tyr Asp
154          290          295          300
156 ttc tgg gcc aaa aag act cga tct cgt atc gtc aat ccg gca aag aga 960
157 Phe Trp Ala Lys Lys Thr Arg Ser Arg Ile Val Asn Pro Ala Lys Arg
158 305          310          315          320
160 gat ctc atg gct cct ctg gag ccg ccg tac tgg ttc ggt acc aag cgc 1008
161 Asp Leu Met Ala Pro Leu Glu Pro Pro Tyr Trp Phe Gly Thr Lys Arg
162          325          330          335
164 tcc cca ctg gag agc gac tac tac gaa atg ctg gac aag ccg agc gtc 1056
165 Ser Pro Leu Glu Ser Asp Tyr Tyr Glu Met Leu Asp Lys Pro Ser Val
166          340          345          350
168 gaa att gtg aat cta gaa caa tcg ccc att gtg gct gtt aca aag aca 1104
169 Glu Ile Val Asn Leu Glu Gln Ser Pro Ile Val Ala Val Thr Lys Thr
170          355          360          365
172 ggt gtg ctc ttg agt gac ggc agc aag agg gaa tgc gac acg atc gtg 1152
173 Gly Val Leu Leu Ser Asp Gly Ser Lys Arg Glu Cys Asp Thr Ile Val
174          370          375          380
176 ctg gcg acg ggt ttc gac agt ttc act ggc tca ttg aca cat atg ggc 1200
177 Leu Ala Thr Gly Phe Asp Ser Phe Thr Gly Ser Leu Thr His Met Gly
178 385          390          395          400
180 ttg aaa aac aag cac gga gtg gac ctg aag gag gtg tgg aaa gat ggc 1248
181 Leu Lys Asn Lys His Gly Val Asp Leu Lys Glu Val Trp Lys Asp Gly
182          405          410          415

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184 ata tct act tat atg gga gtc ttc tct cat ggc ttc ccc aat gcc ttc 1296
185 Ile Ser Thr Tyr Met Gly Val Phe Ser His Gly Phe Pro Asn Ala Phe
186          420          425          430
188 ttc gtc gcc acg gct caa gcc ccg acc gtc ctt tcc aac ggc cca acg 1344
189 Phe Val Ala Thr Ala Gln Ala Pro Thr Val Leu Ser Asn Gly Pro Thr
190          435          440          445
192 atc ata gaa acc caa gtc gac ttg atc gcc gat aca att gca aag ttg 1392
193 Ile Ile Glu Thr Gln Val Asp Leu Ile Ala Asp Thr Ile Ala Lys Leu
194          450          455          460
196 gag gcc gag cac gcc acg tcc gtt gag gcg acg aaa tca gca caa gag 1440
197 Glu Ala Glu His Ala Thr Ser Val Glu Ala Thr Lys Ser Ala Gln Glu
198 465          470          475          480
200 gca tgg tcg att atg att gcc aag atg aac gag cac act ctg ttc ccc 1488
201 Ala Trp Ser Ile Met Ile Ala Lys Met Asn Glu His Thr Leu Phe Pro
202          485          490          495
204 ttg acg gat tcg tgg tgg act gga ggc aac atc cct ggg aaa gca aca 1536
205 Leu Thr Asp Ser Trp Trp Thr Gly Gly Asn Ile Pro Gly Lys Ala Thr
206          500          505          510
208 cgt gct tta acc ttc ata ggc ggg att gct ctc tat gag cag atc tgt 1584
209 Arg Ala Leu Thr Phe Ile Gly Gly Ile Ala Leu Tyr Glu Gln Ile Cys
210          515          520          525
212 caa gag aag gtg gcc aat tgg gat ggg ttt gat gtg ctt cat gct ccc 1632
213 Gln Glu Lys Val Ala Asn Trp Asp Gly Phe Asp Val Leu His Ala Pro
214          530          535          540
216 tgc taa 1638
217 Cys *
218 545
221 <210> SEQ ID NO: 3
222 <211> LENGTH: 545
223 <212> TYPE: PRT
224 <213> ORGANISM: Exophiala spinifera
226 <400> SEQUENCE: 3
227 Met Ser Ala Thr Ser Asn Ser Arg Gly Asp Cys Ser Val Ala Cys Asp
228 1          5          10          15
229 Ala Ile Ile Val Gly Ala Gly Leu Ser Gly Ile Ser Ala Val Tyr Lys
230          20          25          30
231 Leu Arg Lys Leu Arg Leu Asn Ala Lys Ile Phe Glu Gly Ala Pro Asp
232          35          40          45
233 Phe Gly Gly Val Trp His Trp Asn Arg Tyr Pro Gly Ala Arg Val Asp
234          50          55          60
235 Ser Glu Thr Pro Phe Tyr Gln Leu Asn Ile Pro Glu Val Trp Lys Asp
236 65          70          75          80
237 Trp Thr Trp Ser Cys Arg Tyr Pro Asp Gln Lys Glu Leu Leu Ser Tyr
238          85          90          95
239 Val His His Cys Asp Lys Ile Arg Gly Leu Arg Lys Asp Val Tyr Phe
240          100          105          110
241 Gly Ala Glu Val Val Asp Ala Arg Tyr Ala Arg Asp Leu Gly Thr Trp
242          115          120          125
243 Thr Val Lys Thr Ser Ala Gly His Val Ala Thr Ala Lys Tyr Leu Ile

```

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```

244      130      135      140
245 Leu Ala Thr Gly Leu Leu His Arg Lys His Thr Pro Ala Leu Pro Gly
246 145      150      155      160
247 Leu Ala Asp Phe Asn Gly Lys Val Ile His Ser Ser Ala Trp His Glu
248      165      170      175
249 Asp Phe Asp Ala Glu Gly Gln Arg Val Ala Val Ile Gly Ala Gly Ala
250      180      185      190
251 Thr Ser Ile Gln Ile Val Gln Glu Leu Ala Lys Lys Ala Asp Gln Val
252      195      200      205
253 Thr Met Phe Met Arg Arg Pro Ser Tyr Cys Leu Pro Met Arg Gln Arg
254      210      215      220
255 Thr Met Asp Arg Asn Glu Gln Thr Ala Trp Lys Ala Tyr Tyr Pro Thr
256 225      230      235      240
257 Leu Phe Glu Ala Ser Arg Lys Ser Arg Ile Gly Phe Pro Val Gln Ala
258      245      250      255
259 Pro Ser Val Gly Ile Phe Glu Val Ser Pro Glu Gln Arg Glu Ala Tyr
260      260      265      270
261 Phe Glu Glu Leu Trp Glu Arg Gly Ala Phe Asn Phe Leu Ala Cys Gln
262      275      280      285
263 Tyr Arg Glu Val Met Val Asp Lys Lys Ala Asn Arg Leu Val Tyr Asp
264      290      295      300
265 Phe Trp Ala Lys Lys Thr Arg Ser Arg Ile Val Asn Pro Ala Lys Arg
266 305      310      315      320
267 Asp Leu Met Ala Pro Leu Glu Pro Pro Tyr Trp Phe Gly Thr Lys Arg
268      325      330      335
269 Ser Pro Leu Glu Ser Asp Tyr Tyr Glu Met Leu Asp Lys Pro Ser Val
270      340      345      350
271 Glu Ile Val Asn Leu Glu Gln Ser Pro Ile Val Ala Val Thr Lys Thr
272      355      360      365
273 Gly Val Leu Leu Ser Asp Gly Ser Lys Arg Glu Cys Asp Thr Ile Val
274      370      375      380
275 Leu Ala Thr Gly Phe Asp Ser Phe Thr Gly Ser Leu Thr His Met Gly
276 385      390      395      400
277 Leu Lys Asn Lys His Gly Val Asp Leu Lys Glu Val Trp Lys Asp Gly
278      405      410      415
279 Ile Ser Thr Tyr Met Gly Val Phe Ser His Gly Phe Pro Asn Ala Phe
280      420      425      430
281 Phe Val Ala Thr Ala Gln Ala Pro Thr Val Leu Ser Asn Gly Pro Thr
282      435      440      445
283 Ile Ile Glu Thr Gln Val Asp Leu Ile Ala Asp Thr Ile Ala Lys Leu
284      450      455      460
285 Glu Ala Glu His Ala Thr Ser Val Glu Ala Thr Lys Ser Ala Gln Glu
286 465      470      475      480
287 Ala Trp Ser Ile Met Ile Ala Lys Met Asn Glu His Thr Leu Phe Pro
288      485      490      495
289 Leu Thr Asp Ser Trp Trp Thr Gly Gly Asn Ile Pro Gly Lys Ala Thr
290      500      505      510
291 Arg Ala Leu Thr Phe Ile Gly Gly Ile Ala Leu Tyr Glu Gln Ile Cys
292      515      520      525

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/882,694B

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:10; Xaa Pos. 279

Seq#:11; Xaa Pos. 279

VERIFICATION SUMMARY

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Input Set : A:\Seqlist.txt

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L:79 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:312 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:563 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:864 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10
L:934 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:864
L:1228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:272
L:1820 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
L:2018 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:2216 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:2467 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:2718 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24
L:2969 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:3220 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:3471 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
L:3722 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:32